



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/763,976

Source:

IFW0

Date Processed by STIC:

7/12/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand-Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/963,976

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules**, each n or Xaa can **only** represent a single residue. Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be **missing** from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/763,976

DATE: 07/12/2004

TIME: 15:16:58

Input Set : N:\FATIMA\10763976.txt
 Output Set: N:\CRF4\07122004\J763976.raw

3 <110> APPLICANT: Harms, Jerome S.
 4 Splitter, Gary A.
 5 Eakle, Kurt A.
 6 Bremel, Robert D.
 8 <120> TITLE OF INVENTION: Inducible Protein Expression System
 W--> 0 <130> FILE REFERENCE:
 10 <140> CURRENT APPLICATION NUMBER: US 10/763,976
 C--> 11 <141> CURRENT FILING DATE: 2004-07-07
 13 <160> NUMBER OF SEQ ID NOS: 13

ERRORRED SEQUENCES

457 <210> SEQ ID NO: 7
 458 <211> LENGTH: 309
 459 <212> TYPE: PRT
 460 <213> ORGANISM: bovine leukemia virus
 462 <400> SEQUENCE: 7
 464 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys
 E--> 465 1 5 10 5 15 10 15
 467 Pro Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys
 E--> 468 20 25 30
 470 Pro Leu Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp
 E--> 471 35 40 45
 473 Thr Thr His Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp
 E--> 474 50 55 60
 476 Gly Arg Pro Phe Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His
 E--> 477 65 70 75
 479 Val Ser Arg Asp Pro Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn
 E--> 480 80 85 90
 482 Cys Pro Leu Pro Ala Val Arg Ala Gln Pro Gly Pro Val Ser Leu
 E--> 483 95 100 105
 485 Ser Pro Phe Glu Arg Ser Pro Phe Gln Pro Tyr Gln Cys Gln Leu
 E--> 486 110 115 120
 488 Pro Ser Ala Ser Ser Asp Gly Cys Pro Val Ile Gly His Gly Leu
 E--> 489 125 130 135
 491 Leu Pro Trp Asn Asn Leu Val Thr His Pro Cys Pro Arg Lys Val
 E--> 492 140 145 150
 494 Leu Ile Leu Asn Gln Met Ala Asn Phe Ser Leu Leu Pro Pro Phe
 E--> 495 155 160 165
 497 Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser Val Phe Ala Pro
 E--> 498 170 175 180
 500 Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu Leu Thr Leu

Does Not Comply
 Corrected Diskette Needed

see p. 2

misaligned
 amino acid
 number

(see item 3 on
 Error Summary
 sheet)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/763,976

DATE: 07/12/2004

TIME: 15:16:58

Input Set : N:\FATIMA\10763976.txt
 Output Set: N:\CRF4\07122004\J763976.raw

E--> 501 185 190 195
 503 Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe Ser Pro
 E--> 504 200 205 210
 506 Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro Pro
 E--> 507 215 220 225
 509 Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
 E--> 510 230 235 240
 512 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser
 E--> 513 245 250 255
 515 Pro Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln
 E--> 516 260 265 270
 518 Arg Phe Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala
 E--> 519 275 280 285
 521 Ser Arg Lys Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu
 E--> 522 290 295 300
 E--> 524 Glu Asn Glu Trp Leu Ser Arg Leu Phe *** *delete*
 E--> 525 305
 571 <210> SEQ ID NO: 8
 572 <211> LENGTH: 353
 573 <212> TYPE: PRT
 574 <213> ORGANISM: human T-lymphotropic virus 1
 576 <400> SEQUENCE: 8
 579 Met Ala His Phe Pro Gly Phe Gly Gln Ser Leu Leu Phe Gly Tyr
 E--> 580 1 5 10 15
 582 Pro Val Tyr Val Phe Gly Asp Cys Val Gln Gly Asp Trp Cys Pro
 E--> 583 20 25 30
 585 Ile Ser Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu
 E--> 586 35 40 45
 588 Leu Ala Thr Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp
 E--> 589 50 55 60
 591 Gly Arg Val Ile Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu
 E--> 592 65 70 75
 594 Pro Ser Phe Pro Thr Gln Arg Thr Ser Lys Thr Ile Lys Val Leu
 E--> 595 80 85 90
 597 Thr Pro Pro Ile Thr His Thr Thr Pro Asn Ile Pro Pro Ser Phe
 E--> 598 95 100 105
 600 Leu Gln Ala Met Arg Lys Tyr Ser Pro Phe Arg Asn Gly Tyr Met
 E--> 601 110 115 120
 603 Glu Pro Thr Leu Gly Gln His Leu Pro Thr Leu Ser Phe Pro Asp
 E--> 604 125 130 135
 606 Pro Gly Leu Arg Pro Gln Asn Leu Tyr Thr Leu Trp Gly Gly Ser
 E--> 607 140 145 150
 609 Val Val Cys Met Tyr Leu Tyr Gln Leu Ser Pro Pro Ile Thr Trp
 E--> 610 155 160 165
 612 Pro Leu Leu Pro His Val Ile Phe Cys His Pro Gly Gln Leu Gly
 E--> 613 170 175 180
 615 Ala Phe Leu Thr Asn Val Pro Tyr Lys Arg Ile Glu Glu Leu Leu
 E--> 616 185 190 195
 618 Tyr Lys Ile Ser Leu Thr Thr Gly Ala Leu Ile Ile Leu Pro Glu

sane
This misalignment
also occurs
in sequences 2, 3,
and 6

Misaligned
amino acid numbers

see p.3

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/763,976

DATE: 07/12/2004
TIME: 15:16:58

Input Set : N:\FATIMA\10763976.txt
Output Set: N:\CRF4\07122004\J763976.raw

E--> 619 200 205 210
621 Asp Cys Leu Pro Thr Thr Leu Phe Gln Pro Val Arg Ala Pro Val
E--> 622 215 220 225
624 Thr Leu Thr Ala Trp Gln Asn Gly Leu Leu Pro Phe His Ser Thr
E--> 625 230 235 240
627 Leu Thr Thr Pro Gly Leu Ile Trp Thr Phe Thr Asp Gly Thr Pro
E--> 628 245 250 255
630 Met Ile Ser Gly Pro Cys Pro Lys Asp Gly Gln Pro Ser Leu Val
E--> 631 260 265 270
633 Leu Gln Ser Ser Ser Phe Ile Phe His Lys Phe Gln Thr Lys Ala
E--> 634 275 280 285
636 Tyr His Pro Ser Phe Leu Leu Ser His Gly Leu Ile Gln Tyr Ser
E--> 637 290 295 300
639 Ser Phe His Asn Leu His Leu Leu Phe Glu Glu Tyr Thr Asn Ile
E--> 640 305 310 315
642 Pro Ile Ser Leu Leu Phe Asn Lys Lys Glu Ala Asp Asp Asn Asp
E--> 643 320 325 330
645 His Glu Pro Gln Ile Ser Pro Gly Gly Leu Glu Pro Pro Ser Glu
E--> 646 335 340 345
E--> 648 Lys His Phe Arg Glu Thr Glu Val ***
E--> 649 350
685 <210> SEQ ID NO: 9
686 <211> LENGTH: 101
687 <212> TYPE: PRT
688 <213> ORGANISM: human immunodeficiency virus 1
690 <400> SEQUENCE: 9
692 Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly
E--> 693 1 5 10 15
695 Ser Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys
E--> 696 20 25 30
698 Cys Phe His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile
E--> 699 35 40 45
701 Ser Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln
E--> 702 50 55 60
704 Asp Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser
E--> 705 65 70 75
707 Gln Ser Arg Gly Asp Pro Thr Gly Pro Thr Glu Ser Lys Lys
E--> 708 80 85 90
E--> 710 Val Glu Arg Glu Thr Glu Thr Asp Pro Phe Asp ***
E--> 711 95 100

same

same

same

See p. 4 for more info

10/263,976 4

<210> 1
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<221> Promoter
<222> 87..432
<223> BLV Promoter

<220>
<221> misc_feature
<222> 452..576
<223> attR1 Gateway recombination site

<400> 1

This needs explanation in <220>-<223> section.

Give source of
genetic material.

IMPORTANT

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

Also, change all nucleotides from upper-case
letters to
lower-case letters

Since the Sequence Listing is in
"new" Sequence Rule format, use
lower-case letters for nucleotides.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/763,976

DATE: 07/12/2004

TIME: 15:16:59

Input Set : N:\FATIMA\10763976.txt

Output Set: N:\CRF4\07122004\J763976.raw

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:69 M:112 C: (48) String data converted to lower case,
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
M:112 Repeated in SeqNo=2
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:183 M:112 C: (48) String data converted to lower case,
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
M:112 Repeated in SeqNo=3
L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/763,976

DATE: 07/12/2004
TIME: 15:16:59

Input Set : N:\FATIMA\10763976.txt
Output Set: N:\CRF4\07122004\J763976.raw

L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:297 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=4
L:354 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=5
L:411 M:112 C: (48) String data converted to lower case,
L:413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
M:112 Repeated in SeqNo=6
L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:421 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:425 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:429 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:465 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7
L:524 M:342 E: Invalid Stop Code On Error, STOP CODON:
L:525 M:252 E: No. of Seq. differs, <211> LENGTH:Input:309 Found:310 SEQ:7
L:580 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
M:342 Repeated in SeqNo=8
L:649 M:252 E: No. of Seq. differs, <211> LENGTH:Input:353 Found:354 SEQ:8
L:693 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
M:342 Repeated in SeqNo=9
L:711 M:252 E: No. of Seq. differs, <211> LENGTH:Input:101 Found:102 SEQ:9
L:795 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:1189 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=11
L:1530 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=12
L:1872 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=13